

09/990832

GenCore version 5.1.6  
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ON protein - protein search, using sw model

Run on: October 2, 2003, 11:46:19 Search time: 41 seconds  
Database: 27,130 Million cells, updates/week

Title: US-09-990 832c-51

Perfect score: 35

Sequence: 1: SIQVPLP ?

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1107963 seqs, 15870573 residues

Total number of hits satisfying chosen parameters: 110746

Minimum DB seq length: 0

Maximum DB seq length: 230306000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: A\_Geneset\_292003

Result No.	Score	Match	Length	DB ID	Description
1	38	97.4	57	23	AMPOC11 Human GDF1 protein
2	35	95.7	125	21	AM11587 Stromelysin 2-like
3	35	95.7	754	22	AM64352 Stromelysin 2-like
4	34	87.2	164	22	AM65577 Human liver peptid
5	34	87.2	164	22	AM64012 Peptide #1823 enco
6	34	87.2	164	22	AM64012 Peptide #1823 enco
7	34	87.2	164	22	AM64012 Peptide #1823 enco
8	34	87.2	164	22	AM64012 Peptide #1823 enco
9	34	87.2	164	22	AM64012 Peptide #1823 enco

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being plotted, and is derived by analysis of the total score distribution.

SUMMARIES

1	34	87.2	164	22	AM14102 Peptide #8045 enco
2	34	87.2	164	22	AM14102 Peptide #8045 enco
3	34	87.2	164	22	AM14102 Peptide #8045 enco
4	34	87.2	164	22	AM14102 Peptide #8045 enco
5	34	87.2	164	22	AM14102 Peptide #8045 enco
6	34	87.2	164	22	AM14102 Peptide #8045 enco
7	34	87.2	164	22	AM14102 Peptide #8045 enco
8	34	87.2	164	22	AM14102 Peptide #8045 enco
9	34	87.2	164	22	AM14102 Peptide #8045 enco
10	34	87.2	164	22	AM14102 Peptide #8045 enco
11	34	87.2	164	22	AM14102 Peptide #8045 enco
12	34	87.2	164	22	AM14102 Peptide #8045 enco
13	34	87.2	164	22	AM14102 Peptide #8045 enco
14	34	87.2	164	22	AM14102 Peptide #8045 enco
15	34	87.2	164	22	AM14102 Peptide #8045 enco
16	34	87.2	164	22	AM14102 Peptide #8045 enco
17	34	87.2	164	22	AM14102 Peptide #8045 enco
18	34	87.2	164	22	AM14102 Peptide #8045 enco
19	34	87.2	164	22	AM14102 Peptide #8045 enco
20	34	87.2	164	22	AM14102 Peptide #8045 enco
21	34	87.2	164	22	AM14102 Peptide #8045 enco
22	34	87.2	164	22	AM14102 Peptide #8045 enco
23	34	87.2	164	22	AM14102 Peptide #8045 enco
24	34	87.2	164	22	AM14102 Peptide #8045 enco
25	34	87.2	164	22	AM14102 Peptide #8045 enco
26	34	87.2	164	22	AM14102 Peptide #8045 enco
27	34	87.2	164	22	AM14102 Peptide #8045 enco
28	34	87.2	164	22	AM14102 Peptide #8045 enco
29	34	87.2	164	22	AM14102 Peptide #8045 enco
30	34	87.2	164	22	AM14102 Peptide #8045 enco
31	34	87.2	164	22	AM14102 Peptide #8045 enco
32	34	87.2	164	22	AM14102 Peptide #8045 enco
33	34	87.2	164	22	AM14102 Peptide #8045 enco
34	34	87.2	164	22	AM14102 Peptide #8045 enco
35	34	87.2	164	22	AM14102 Peptide #8045 enco
36	34	87.2	164	22	AM14102 Peptide #8045 enco
37	34	87.2	164	22	AM14102 Peptide #8045 enco
38	34	87.2	164	22	AM14102 Peptide #8045 enco
39	34	87.2	164	22	AM14102 Peptide #8045 enco
40	34	87.2	164	22	AM14102 Peptide #8045 enco
41	34	87.2	164	22	AM14102 Peptide #8045 enco
42	34	87.2	164	22	AM14102 Peptide #8045 enco
43	34	87.2	164	22	AM14102 Peptide #8045 enco
44	34	87.2	164	22	AM14102 Peptide #8045 enco
45	34	87.2	164	22	AM14102 Peptide #8045 enco

AL-GHRI-MIS

1	34	87.2	164	22	AM14102 Peptide #8045 enco
2	34	87.2	164	22	AM14102 Peptide #8045 enco
3	34	87.2	164	22	AM14102 Peptide #8045 enco
4	34	87.2	164	22	AM14102 Peptide #8045 enco
5	34	87.2	164	22	AM14102 Peptide #8045 enco
6	34	87.2	164	22	AM14102 Peptide #8045 enco
7	34	87.2	164	22	AM14102 Peptide #8045 enco
8	34	87.2	164	22	AM14102 Peptide #8045 enco
9	34	87.2	164	22	AM14102 Peptide #8045 enco
10	34	87.2	164	22	AM14102 Peptide #8045 enco
11	34	87.2	164	22	AM14102 Peptide #8045 enco
12	34	87.2	164	22	AM14102 Peptide #8045 enco
13	34	87.2	164	22	AM14102 Peptide #8045 enco
14	34	87.2	164	22	AM14102 Peptide #8045 enco
15	34	87.2	164	22	AM14102 Peptide #8045 enco
16	34	87.2	164	22	AM14102 Peptide #8045 enco
17	34	87.2	164	22	AM14102 Peptide #8045 enco
18	34	87.2	164	22	AM14102 Peptide #8045 enco
19	34	87.2	164	22	AM14102 Peptide #8045 enco
20	34	87.2	164	22	AM14102 Peptide #8045 enco
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25	34	87.2	164	22	AM14102 Peptide #8045 enco
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33	34	87.2	164	22	AM14102 Peptide #8045 enco
34	34	87.2	164	22	AM14102 Peptide #8045 enco
35	34	87.2	164	22	AM14102 Peptide #8045 enco
36	34	87.2	164	22	AM14102 Peptide #8045 enco
37	34	87.2	164	22	AM14102 Peptide #8045 enco
38	34	87.2	164	22	AM14102 Peptide #8045 enco
39	34	87.2	164	22	AM14102 Peptide #8045 enco
40	34	87.2	164	22	AM14102 Peptide #8045 enco
41	34	87.2	164	22	AM14102 Peptide #8045 enco
42	34	87.2	164	22	AM14102 Peptide #8045 enco
43	34	87.2	164	22	AM14102 Peptide #8045 enco
44	34	87.2	164	22	AM14102 Peptide #8045 enco
45	34	87.2	164	22	AM14102 Peptide #8045 enco

RESULT 1

APP0611

XX APP0611 standard: Protein: 57 AA

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CC discloses genomic DNA sequences (AB016170-AB016511), expressed DNA  
CC sequences (AB01640-AB016175) and the encoded proteins  
CC (AB016270-AB016292) for this patent, did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pat\_sequences.  
XX  
XX Sequence 754 AA:  
Query Match 89.7% Score 35, DB 22, Length 754:  
Best Local Similarity 100.0%: Pred. No. 1, 2nd 0:  
Matches 6: Conservative 0: Mismatches 0: Indels 0: Gaps 0  
QY 2 ISYPLP 7  
DB 143 ISYPLP 145  
RESULT 4  
AB055577  
ID AB055577 standard: Peptide: 154 AA.  
AC ABC55577:  
XX  
XX 25-FEB-2003 (first entry)  
XX Human liver peptide, SEQ ID NO 34225.  
XX Human: liver: cirrhosis; hyperlipoproteinemia; hyperlipidaemia;  
XX hypercholesterolaemia; coronary heart disease.  
XX Homo sapiens.  
XX  
XX W02015727-A2.  
XX 09-AUG-2001.  
XX 10-JAN-2001: 200US-020664.  
XX 04-FEB-2001: 200US-0180312.  
XX 26-MAY-2001: 200US-0207455.  
XX 30-JUN-2001: 200US-0606408.  
XX 03-AUG-2001: 200US-0632766.  
XX 21-SEP-2001: 200US-0234787.  
XX 27-SEP-2001: 200US-0235159.  
XX 04-OCT-2001: 200US-0024261.  
XX (MOLB) MOLECULAR DYNAMICS INC.  
XX Patm SG, Hanzel DK, Chan W, Rank DR.  
XX WPI: 2601-48495/61.  
XX  
XX Human genome-derived single exon nucleic acid probes useful for  
XX analysing gene expression in human adult liver.  
XX  
XX Claim 27: SEQ ID NO 34225: 659pp: English.  
XX The invention relates to a single exon nucleic acid probe (SEQ ID: 1) for  
XX measuring human gene expression in a sample derived from human adult  
XX liver, comprising one of 11,69 defined nucleotide sequences listed in  
XX Table 1, which are complementary to a nucleic acid molecule expressed in the  
XX liver. (1) may be used for predicting, measuring and displaying gene  
XX expression in samples derived from human adult liver. The genes  
XX identified may be involved in genetic liver diseases such as cirrhosis,  
XX hyperlipoproteinemia, hyperlipidaemia and hypercholesterolaemia which  
XX is associated with coronary heart disease. AB047348-AB055910 represent  
XX human liver: single exon encoded peptides of the invention.  
XX Note: The sequence information for this patent does not appear in the  
XX printed specification but was obtained in electronic format directly  
XX from WIPO at ftp.wipo.int/pub/published\_pat\_sequences.

SV Sequence 154 AA:  
Query Match 91.2% Score 34, DB 22, Length 154:  
Best Local Similarity 100.0%: Pred. No. 1, 2nd 0:  
Matches 3: Conservative 2: Mismatches 0: Indels 0: Gaps 0:  
QY 1 ISYPLP 7  
DB 52 ALSYPLP 98  
RESULT 5  
AB040317  
ID AB040317 standard: Peptide: 154 AA  
AC AB040317:  
XX  
XX 04-FEB-2002 (first entry)  
XX Peptide: 17821 encoded by human foetal liver single exon probe.  
XX Human: foetal liver: gene expression: single exon nucleic acid probe  
XX Homo sapiens.  
XX  
XX W02015727-A2.  
XX 09-AUG-2001.  
XX 10-JAN-2001: 200US-020664.  
XX 04-FEB-2001: 200US-0180312.  
XX 26-MAY-2001: 200US-0207455.  
XX 30-JUN-2001: 200US-0606408.  
XX 03-AUG-2001: 200US-0632766.  
XX 21-SEP-2001: 200US-0234787.  
XX 27-SEP-2001: 200US-0235159.  
XX 04-OCT-2001: 200US-0024261.  
XX (MOLB) MOLECULAR DYNAMICS INC.  
XX Patm SG, Hanzel DK, Chan W, Rank DR.  
XX WPI: 2601-48495/62.  
XX  
XX Human genome-derived single exon nucleic acid probes useful for  
XX analysing gene expression in human foetal liver.  
XX  
XX Claim 27: SEQ ID NO 14562: 635pp: English.  
XX The invention relates to a single exon nucleic acid probe for  
XX measuring human gene expression in a sample derived from human foetal  
XX liver. The single exon nucleic acid probes may be used for predicting,  
XX measuring and displaying gene expression in samples derived from human  
XX foetal liver. The present sequence is a peptide encoded by a single exon  
XX nucleic acid probe of the invention.  
XX Note: The sequence data for this patent did not form part of the  
XX printed specification, but was obtained in electronic format directly  
XX from WIPO at ftp.wipo.int/pub/published\_pat\_sequences.  
XX  
XX Sequence 154 AA:  
Query Match 87.2% Score 34, DB 22, Length 154:  
Best Local Similarity 100.0%: Pred. No. 1, 2nd 0:  
Matches 5: Conservative 2: Mismatches 0: Indels 0: Gaps 0:  
QY 1 ISYPLP 7  
DB 52 ALSYPLP 98  
RESULT 6  
AB024716







PT Cytokine-like factor 1 (CLF-1) and interleukin (IL-6/60) complexes,  
 PT polypeptides, and nucleic acids, useful in research, diagnosis and for  
 PT treating inflammatory and autoimmune disorders.

XX Claim 1: Page 15-16: 67pp. English.

CC The present sequence is that of human interleukin-B60 (IL-6/60), a  
 CC novel, small, soluble cytokine-like protein that exhibits structural  
 CC motifs characteristic of a member of the long-chain cytokines and  
 CC which shows homology to granulocyte colony stimulating factor and  
 CC interleukin-6. IL-6/60 may have either stimulatory or inhibitory  
 CC effects on haematopoietic cells, including e.g. lymphoid cells,  
 CC such as T-cells, B-cells, natural killer cells, macrophages,  
 CC dendritic cells, haematopoietic progenitors, etc. Methods are  
 CC provided for modulating the physiology or development of a cell or  
 CC tissue culture cells by contacting the cell with an agonist or  
 CC antagonist of IL-6/60 or an agonist or antagonist of a complex of  
 CC factor in a complex of IL-6/60 and its purifier. Cytokine serves as a key physiological  
 CC factor in neuron development and regeneration. IL-6/60, its  
 CC agonists and antagonists may be used to treat inflammatory or  
 CC autoimmune disorders and also for drug screening.

XX Sequence 2:5 AA:

Query Match 87.2%, Score 34: DB 21: Length 215;  
 Best Local Similarity 71.4%, Pred. No. 1:5e-02;  
 Matches 5: Conservative 2: Mismatches 0: Indels 0: Gaps 0:

QY 1 SUSHIP 7

DB 143 ALGYP.P 149

RESULT 13

AA019587  
 ID AA019587 standard; Protein: 215 AA.

XX AA019587:

XX 22-JAN-2001 (first entry)

XX Mouse interleukin-B60 (IL-6/60).

XX Interleukin-B60; IL-6/60; mouse; cytokine; cytokine-like factor-1;  
 XX haematopoietic; inflammation; anti-inflammatory; autoimmune disease;  
 XX therapy.

XX Mus musculus.

XX Key Location/Qualifiers

XX Peptide 1-17

XX Protein /label: Signal\_peptide

XX 18-215

XX /label: Mature-protein

XX W0200003631-A1.

XX 14-SEP-2000.

XX 05-MAR-2000; 2000MG:JSG5:62

XX 11-MAR-1999; 99CS:0267401

XX (SCHE); SCHERING CORP.

XX Oppmann B, Timans JC, Kasteler PA, Bazan JF;

XX WPI: 2003-567425/55

XX N-PS08; AAA0547.

XX Cytokine-like factor 1 (CLF-1) and interleukin (IL)-6/60 complexes  
 XX polypeptides, and nucleic acids, useful in research, diagnosis and for  
 XX treating inflammatory and autoimmune disorders.

PT Treating inflammatory and autoimmune disorders.  
 XX Claim 1: Page 17: 67pp. English.

CC The present sequence is that of mouse interleukin B60 (IL-B60), a  
 CC novel, small, soluble cytokine-like protein that exhibits structural  
 CC motifs characteristic of a member of the long-chain cytokines and  
 CC which shows homology to granulocyte colony stimulating factor and  
 CC interleukin-6. IL-B60 may have either stimulatory or inhibitory  
 CC effects on haematopoietic cells, including e.g. lymphoid cells,  
 CC such as T-cells, B-cells, natural killer cells, macrophages,  
 CC dendritic cells, haematopoietic progenitors, etc. Methods are  
 CC provided for modulating the physiology or development of a cell or  
 CC tissue culture cells by contacting the cell with an agonist or  
 CC antagonist of IL-B60 or an agonist or antagonist of a complex of  
 CC factor in a complex of IL-B60 and its purifier. Cytokine serves as a key physiological  
 CC factor in neuron development and regeneration. IL-B60, its  
 CC agonists and antagonists may be used to treat inflammatory or  
 CC autoimmune disorders and also for drug screening.

XX Sequence 2:5 AA:

Query Match 87.2%, Score 34: DB 21: Length 215;  
 Best Local Similarity 71.4%, Pred. No. 1:5e-02;  
 Matches 5: Conservative 2: Mismatches 0: Indels 0: Gaps 0:

QY 1 SUSHIP 7

DB 143 ALGYP.P 149

RESULT 14

AA019587  
 ID AA019587 standard; Protein: 223 AA.

XX AA019587:

XX 02-JUL-2001 (first entry)

XX Human cardiotrophin-like cytokine (CLC) protein

XX Human, biologically active complex; haemopoietin receptor; NR6;  
 XX cardiotrophin-like cytokine; CLC; therapy; prophylaxis; proliferation;  
 XX differentiation; cell survival; neurotrophic activity.

XX Homo sapiens

XX Key Location/Qualifiers

XX Peptide 1-17

XX Protein /label: Signal\_peptide

XX 18-223

XX /label: Human mature CLC-protein

XX /note: "Cardiotrophin-like cytokine"

XX W0200127157-A1

XX 19-MAR-2001.

XX 06-SEP-2000; 2000MG:AM01116.

XX 06-SEP-1999; 99AU:0303722.

XX 12-MAY-2000; 2000MG:0307463.

XX (ANSA); ANSAD OPERATIONS PTY LTD.

XX Nish A, Chou KM, Puri LJ, Reid K, Bartlett PE, Hilton DJ;

XX Nakata Y, Hasegawa M

XX WPI: 2001-740787/29

XX N-PS08; AM01201.

XX New biologically active complex comprising NR6 and

PT cardiostrophin-like cytokine, for facilitating proliferation.  
 PT differentiation and/or survival of a cell.  
 PA Claim 32: Page 114-115: 12pp: English.  
 XX The present invention relates to a biologically active complex comprising  
 CC a hemopoietin receptor, and cardiostrophin-like cytokine (CLC).  
 CC The complex is useful in the manufacture of a medicament for the  
 CC treatment and/or prophylaxis of a subject, as it is involved in  
 CC facilitating proliferation, differentiation and/or survival of a cell.  
 CC The complex or its components have neurotrophic activity. The present  
 CC sequence is human cardiostrophin-like cytokine (CLC) protein.  
 XX Sequence 223 AA.  
 Query Match: 47.2%, Score 34, 25.22, Length 223  
 Best Local Similarity: 71.4%, Pred. No. 1.6e+02,  
 Matches 5: Conservative 2: Mismatches 6: Indels 0: Gaps 0  
 QY 1 SIGYPLP 7  
 DB 153 AAGYPLP 153  
 RESULT 15  
 AA29715  
 AA29715 Standard Protein: 225 AA.  
 AC AA29715:  
 DT 05-NOV-1998 (first entry)  
 DE Human neurotrophic factor NNT-1.  
 KW NNT-1: neurotrophic factor; human; anti-inflammatory; adjuvant.  
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease;  
 KW amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome;  
 KW congenital deafness; congenital blindness; congenital deafness;  
 KW congenitally immunodeficiency; X-linked adrenoleukodystrophy;  
 KW hypogammaglobulinemia; X-linked agammaglobulinemia; antisepsis;  
 KW therapy.  
 XX Homo sapiens.  
 FS Key Location/Qualifiers  
 FH Peptide 1..27  
 FI Label= Sig\_pept.db  
 FI Protein 28..225  
 FI Label= Mat\_protein  
 XX WC9813922-A1.  
 XX 06-AUG-1998.  
 XX 02-FEB-1998: 98WO-US92163.  
 XX 30-JAN-1998: 98US-0016334.  
 XX 03-FEB-1997: 97US-0792015.  
 XX (AMGE); AMGEN INC.  
 XX Chong W. Elliot GS. Sarniento H. Senaldi G.  
 XX NFI: 1998-437475/37.  
 XX N-PSDB: AAV47510, AAV47511.  
 XX Newly isolated nucleic acid encoding human or murine neurotrophic  
 XX factor NNT-1 - useful for treatment of neurological, and  
 XX immunological diseases or inflammation, also as vaccine adjuvant.  
 XX Claim 12: Fig 1, 12pp: English.  
 XX This is the amino acid sequence of a novel neurotrophic factor.

CC designated NNT-1, that is a growth factor for neurons and for H or  
 CC cells. It was deduced from isolated cDNA (see AAV47510) and  
 CC genomic DNA (see AAV47511) clones containing the cDNA or  
 CC genomic DNA. The cDNA and genomic DNA clones were obtained  
 CC of NNT-1 polypeptides. These are used to treat: (i) neurological  
 CC or immunological diseases, specifically Alzheimer's, Parkinson's  
 CC or Huntington's disease, amyotrophic lateral sclerosis,  
 CC Charcot-Marie-Tooth syndrome, peripheral neuropathy, dystrophy and  
 CC degeneration of the neural retina, or conditions characterised by  
 CC or B cell defects, e.g. common variable immunodeficiency (CVID),  
 CC selective IgA deficiency, hypogammaglobulinemia and X-linked  
 CC agammaglobulinemia (claimed), but many others disclosed; and (ii)  
 CC inflammation. NNT-1 is also able to boost immunoreactivity and  
 CC antibody production following vaccination, and, since it inhibits  
 CC tumour growth, it is useful in cancer therapy. NNT-1 may also  
 CC be used as a vaccine adjuvant. Cells that have been engineered to  
 CC express NNT-1 can be implanted, or nucleic acids are delivered in  
 CC gene therapy vectors.  
 XX Sequence 225 AA.  
 Query Match: 47.2%, Score 34, 25.22, Length 225.  
 Best Local Similarity: 71.4%, Pred. No. 1.6e+02,  
 Matches 5: Conservative 2: Mismatches 6: Indels 0: Gaps 0  
 QY 1 SIGYPLP 7  
 DB 153 AAGYPLP 153  
 Seq. B. Computed: Method: 2: 2003: 13:55:02  
 Job time: 1:43 secs







```

1 NUMBER OF SEQ ID NOS: 24
2 SEQ ID NO. 2
3 LENGTH: 245
4 TYPE: PRT
5 ORGANISM: homo sapiens
6 FEATURE:
7 NAME/KEY: signal
8 LOCATION: (271..11)
9 FEATURE:
10 NAME/KEY: polypeptide
11 LOCATION: (1..198)
12 OS: 10-112-793.2
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1 SOFTWARE: AccuTax Sequence Listing Engine - vers. 1.1
2 SEQ ID NO: 7614
3 LENGTH: 47
4 TYPE: PRT
5 ORGANISM: Homo sapiens
6 FEATURE:
7 OTHER INFORMATION: MAP TO AF043945.1
8 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6.7
9 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 6.9
10 OTHER INFORMATION: EXPRESSED IN PANCREAS, SIGNAL = 6.7
11 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 6.6
12 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 6.9
13 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 7.4
14 OTHER INFORMATION: EXPRESSED IN HEL-30, SIGNAL = 8.1
15 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
16 OTHER INFORMATION: EXPRESSED IN BT47A, SIGNAL = 6
17 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 8
18 OTHER INFORMATION: EST_HUMAN HIT: A120798C.1, EVALUOF 2.20E+00
19 OTHER INFORMATION: SWISSPROT HIT: F1101, EVALUOE 8.10E+00
20 US-C9364-761-7614
21 Query Match: 84.6%; Score 35; DB %; Length 47;
22 Best Local Similarity: 71.4%; Pred NC 2%;
23 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
24 QY 1: SLVFLF 7
25 DE 22 SVFFLF 24
26 RESULT 7
27 % Seq-ID No: 7614-7614-22
28 Sequence: 22: Application, US/C9375694
29 Patent No: US20020065710A1
30 GENERAL INFORMATION:
31 APPLICANT: Glucksmann, Maria A.
32 TITLE OF INVENTION: 20685, 579, 171.4, 2282, 13894, and
33 FILE REFERENCE: 32613, No US20020068710A1e Human Transporters
34 CURRENT APPLICATION NUMBER: US/02/755,654
35 PRIORITY CLAIMING DATE: 2000/12/29
36 PRIOR APPLICATION NUMBER: 56/185,306
37 PRIOR FILING DATE: 2000/12/29
38 NUMBER OF SEQ IN NOS: 42
39 SOFTWARE: FASTSEQ for Windows Version 4.0
40 SEQ ID NO: 22
41 LENGTH: 600
42 TYPE: PRT
43 ORGANISM: Artificial Sequence**
44 FEATURES:
45 OTHER INFORMATION: Pfam Consensus Sequence
46 US-09-752 693-72
47 Query Match: 84.5%; Score 31; DB %; Length 602;
48 Best Local Similarity: 83.3%; Pred. NC 4.5E+C2;
49 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
50 QY 2 IGVFLP 7
51 DE 17C IGVFLP 17S
52 RESULT 8
53 GS-13-145-215-22
54 Sequence: 22: Application 95/0156239
55 Publication No.: 952003016374A1
56 GENERAL INFORMATION:
57 APPLICANT: Glucksmann, Maria A.
58 APPLICANT: Appleier, Catherine,
59 TITLE OF INVENTION: Affixes Molecule-Like Sequences Encoded Human
60 TITLE OF INVENTION: Affixes Molecule-Like Molecule
61 TITLE OF INVENTION: Affixes Molecule-Like Enzyme-Like Molecule, and Uses Thereof
62 FILE REFERENCE: 55802/2247345

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1 SOFTWARE: AccuTax Sequence Listing Engine - vers. 1.1
2 SEQ ID NO: 7614
3 LENGTH: 47
4 TYPE: PRT
5 ORGANISM: Homo Sapiens
6 FEATURE:
7 OTHER INFORMATION: MAP TO AF043945.1
8 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6.7
9 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 6.9
10 OTHER INFORMATION: EXPRESSED IN PANCREAS, SIGNAL = 6.7
11 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 6.6
12 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 6.9
13 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 7.4
14 OTHER INFORMATION: EXPRESSED IN HEL-30, SIGNAL = 8.1
15 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
16 OTHER INFORMATION: EXPRESSED IN BT47A, SIGNAL = 6
17 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 8
18 OTHER INFORMATION: EST_HUMAN HIT: A120798C.1, EVALUOF 2.20E+00
19 OTHER INFORMATION: SWISSPROT HIT: F1101, EVALUOE 8.10E+00
20 US-C9364-761-7614
21 Query Match: 84.6% Score 35, DB %; Length 47;
22 Best Local Similarity: 71.4%; Pred NC 2%;
23 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
24 QY 1: SLVFLF 7
25 DE 22 SVFFLF 24
26 RESULT 7
27 % Seq=7614-7614-22
28 Sequence=22: Application, US/C9375694
29 Patent No. US20020065710A1
30 GENERAL INFORMATION:
31 APPLICANT: Glucksmann, Maria A.
32 TITLE OF INVENTION: 20685, 579, 171.4, 2282, 10894, and
33 FILE REFERENCE: 32613, No US20020068710A1e Human Transporters
34 CURRENT APPLICATION NUMBER: US/02/755,654
35 PRIORITY CLAIMING NUMBER: 031-56188
36 PRIOR APPLICATION NUMBER: 56/185,306
37 PRIOR FILING DATE: 2000-12-29
38 NUMBER OF SEQ IN NOS: 42
39 SOFTWARE: FASTSEQ for Windows Version 4.0
40 SEQ ID NO 22
41 LENGTH: 600
42 TYPE: PRT
43 ORGANISM: Artificial Sequence**
44 FEATURES:
45 OTHER INFORMATION: Pfam Consensus Sequence
46 US-09-752-693-22
47 Query Match: 84.5% Score 31; DB %; Length 602;
48 Best Local Similarity: 83.3%; Pred. No. 4-5e-C2;
49 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
50 QY 2 IGVFLP 7
51 DE 17C IGVFLP 17S
52 RESULT 8
53 GS-13-145-215-22
54 Sequence=22: Application 95/0156239
55 Publication No.: 952003036374A1
56 GENERAL INFORMATION:
57 APPLICANT: Glucksmann, Maria A.
58 APPLICANT: Appleier, Catherine,
59 TITLE OF INVENTION: ATPase-Molecule, A Human Ubiquitin-Like Molecule
60 NUMBER OF SEQUENCES: 1
61 FILE REFERENCE: 55802/2247345

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US-10-156-239-22

Query Match: 84.68: Score 33: DB 15: Length 602:  
Best Local Similarity 83.38: Pred. NO. 4.6e+02:  
Matches 5: Conservative 1: Mismatches 0: Indels 0: Gaps 0:

CY 2 IGVDP 7  
DB 170 IGVDP 175

RESULT 9  
US-10-199-485-22  
Sequence 22: Application US/0199485  
Publication NO. US20030077626A1  
GENERAL INFORMATION:  
APPLICANT: Glucksmann, Maria A.  
TITLE OF INVENTION: 23613 NO. US20030077626A1 and Human Transporters  
FILE REFERENCE: 35660/249468 NO. US20030077626A1 and Human Transporters  
CURRENT APPLICATION NUMBER: US/10/199-485  
CURRENT FILING DATE: 2002-07-18  
PRIOR APPLICATION NUMBER: 69/795,693  
PRIOR FILING DATE: 2001-02-26  
PRIOR FILING DATE: 2001-02-26  
PRIOR FILING DATE: 2000-02-29  
SUPERIOR OF SEQ ID NOS: 42  
SEQ ID NO: 2  
LENGTH: 602  
TYPE: PPT  
FEATURE:  
OTHER INFORMATION: Pfam Consensus sequence  
US-10-156-239-22

US-10-156-239-22

Query Match: 84.68: Score 33: DB 15: Length 602:  
Best Local Similarity 83.38: Pred. NO. 4.6e+02:  
Matches 5: Conservative 1: Mismatches 0: Indels 0: Gaps 0:

CY 2 IGVDP 7  
DB 170 IGVDP 175

RESULT 10  
US-10-199-485-22  
Sequence 22: Application US/0199485  
Publication NO. US20030077626A1  
GENERAL INFORMATION:  
APPLICANT: Glucksmann, Maria A.  
TITLE OF INVENTION: 23613 NO. US20030077626A1 and Human Transporters  
FILE REFERENCE: 35660/249468 NO. US20030077626A1 and Human Transporters  
CURRENT APPLICATION NUMBER: US/10/199-485  
CURRENT FILING DATE: 2002-07-18  
PRIOR APPLICATION NUMBER: 69/795,693  
PRIOR FILING DATE: 2001-02-26  
PRIOR FILING DATE: 2001-02-26  
PRIOR FILING DATE: 2000-02-29  
SUPERIOR OF SEQ ID NOS: 42  
SEQ ID NO: 2  
LENGTH: 602  
TYPE: PPT  
FEATURE:  
OTHER INFORMATION: Pfam Consensus sequence  
US-10-199-485-22

US-09-990-832c-51

Sequence 19: Application US/0999556  
Publication NO. US20030176319A1  
GENERAL INFORMATION:  
APPLICANT: Cooper, Bruce A.  
TITLE OF INVENTION: 11 C-terminal Processing Proteases: Methods for Thrombin  
TITLE OF INVENTION: STRUCTURAL DETERMINATION AND RATIONAL INHIBITOR DESIGN  
FILE REFERENCE: 01-07-15 NA  
CURRENT APPLICATION NUMBER: US/09/999-832c  
CURRENT FILING DATE: 2001-11-15  
PRIOR APPLICATION NUMBER: 60/185,506  
PRIOR FILING DATE: 2000-02-26  
SUPERIOR OF SEQ ID NOS: 175  
SEQ ID NO: 9  
LENGTH: 602  
TYPE: PPT  
FEATURE:  
OTHER INFORMATION: Pfam Consensus sequence  
US-09-990-832c-51

US-09-990-832c-51

Query Match: 84.68: Score 33: DB 15: Length 602:  
Best Local Similarity 83.38: Pred. NO. 4.6e+02:  
Matches 5: Conservative 1: Mismatches 0: Indels 0: Gaps 0:

CY 2 IGVDP 7  
DB 170 IGVDP 175

RESULT 11  
US-10-297-895A-20  
Sequence 20: Application US/10297895A  
Publication NO. US20030176319A1  
GENERAL INFORMATION:  
APPLICANT: Glucksmann, Maria A.  
TITLE OF INVENTION: 23613 NO. US20030176319A1 and its DNA  
FILE REFERENCE: 2740 US/P  
CURRENT APPLICATION NUMBER: US/10/297-895A  
CURRENT FILING DATE: 2002-12-10  
PRIOR APPLICATION NUMBER: 60/185,506  
PRIOR FILING DATE: 2000-06-22  
PRIOR APPLICATION NUMBER: NP 2001-122125  
PRIOR FILING DATE: 2001-06-20  
SUPERIOR OF SEQ ID NOS: 22  
SEQ ID NO: 673  
LENGTH: 673  
TYPE: PPT  
FEATURE:  
OTHER INFORMATION: Pfam Consensus sequence  
US-10-297-895A-20

US-10-297-895A-20

Query Match: 84.68: Score 33: DB 15: Length 673:  
Best Local Similarity 83.38: Pred. NO. 8e+02:  
Matches 5: Conservative 0: Mismatches 1: Indels 0: Gaps 0:

CY 2 IGVDP 7  
DB 170 IGVDP 175

RESULT 12  
US-10-297-895A-10  
Sequence 10: Application US/10297895A  
Publication NO. US20030176319A1  
GENERAL INFORMATION:  
APPLICANT: Glucksmann, Maria A.  
TITLE OF INVENTION: 23613 NO. US20030176319A1 and its DNA  
FILE REFERENCE: 2740 US/P  
CURRENT APPLICATION NUMBER: US/10/297-895A  
CURRENT FILING DATE: 2002-12-10  
PRIOR APPLICATION NUMBER: 60/185,506  
PRIOR FILING DATE: 2001-06-20  
SUPERIOR OF SEQ ID NOS: 22  
SEQ ID NO: 673  
LENGTH: 673  
TYPE: PPT  
FEATURE:  
OTHER INFORMATION: Pfam Consensus sequence  
US-10-297-895A-10

1 PRIOR APPLICATION NUMBER: JP 2601-122125  
2 PRIOR FILING DATE: 2001-04-20  
3 NUMBER OF SEQ ID NOS: 22  
4 SEQ ID NO 10  
5 LENGTH: 927  
6 TYPE: PRT Human  
7 ORGANISM: HUMAN  
8 US-10-297-895A.10

Query Match 42.1% Score 32: DB 12, Length 427,  
Best Local Similarity 85.7% Pctd No. 11e-C32  
Matches 6: Conservative 0: Mismatches 1: Indels 0: Gaps 0:

QY 1 SIGPEP 7

DB 119 SIGPEP 135

RESULT 13

US-09-919-408-2  
1 Sequence 2: Application US/09/01408  
2 Patent No. US2004072077A1  
3 GENERAL INFORMATION:  
4 APPLICANT: LAMARCA, JON R  
5 TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL  
6 TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS  
7 NUMBER OF SEQUENCES: 10  
8 CORRESPONDENCE ADDRESS:  
9 ADDRESS: 180 VADICK STREET  
10 STREET: 180 VADICK STREET  
11 CITY: New York  
12 STATE: New York  
13 COUNTRY: U.S.A.  
14 ZIP: 10014

COMPUTER READABLE FORM:  
1 MEDIUM TYPE: floppy disk  
2 COMPUTER: IBM PC COMPATIBLE  
3 OPERATING SYSTEM: PC DOS/MS-DOS  
4 SOFTWARE: PATENT RELEASE #1.0, Version #1.25  
5 CURRENT APPLICATION DATA:  
6 APPLICATION NUMBER: US/09/01408  
7 FILING DATE: 11-Jul-2001

CLASSIFICATION: (Unknown)  
1 APPLICATION DATA:  
2 FILING DATE: 07/07/95  
3 APPLICATION NUMBER: US 07/496 397  
4 FILING DATE: 26-JUN-1992  
5 APPLICATION NUMBER: US PCT/US92/05401  
6 FILING DATE: 26-JUN-1992  
7 FILING DATE: 15-APR-1992  
8 APPLICATION NUMBER: US PCT/US92/02750  
9 FILING DATE: 02-APR-1992  
10 APPLICATION NUMBER: US 07/413 593  
11 FILING DATE: 24-DEC-1991  
12 APPLICATION NUMBER: US 07/793 365  
13 FILING DATE: 15-NOV-1991  
14 APPLICATION NUMBER: US 07/728 913  
15 FILING DATE: 28-JUN-1991  
16 APPLICATION NUMBER: US 07/673 666  
17 FILING DATE: 02-APR-1991

ATTORNEY/AGENT INFORMATION:  
1 NAME: Feit, Irvin N.  
2 REGISTRATION NUMBER: 28 601  
3 REFERENCE/DOCKET NUMBER: LEM-1-7P  
4 TELECOMMUNICATION INFORMATION:  
5 TELEPHONE: 212-645-1405  
6 TELEFAX: 212-645-2054

INFORMATION FOR SEQ ID NO: 2:  
1 SEQUENCE CHARACTERISTICS:  
2 LENGTH: 992 amino acids  
3 TYPE: amino acid

1 Molecule Type: PRTail  
2 SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
3 US-09-919-408-2  
4 Query Match 82.1% Score 32: DB 9, Length 592,  
5 Best Local Similarity 80.7% Pctd No. 11e-C32  
6 Matches 9: Conservative 0: Mismatches 1: Indels 0: Gaps 0:

QY 1 SIGPEP 7  
DB 456 SIGPEP 481

RESULT 14

US-09-919-408-2  
1 Sequence 2: Application US/09/01408  
2 Patent No. US2004072077A1  
3 GENERAL INFORMATION:  
4 APPLICANT: LAMARCA, JON R  
5 TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL  
6 TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS  
7 NUMBER OF SEQUENCES: 10  
8 CORRESPONDENCE ADDRESS:  
9 ADDRESS: 180 VADICK STREET  
10 STREET: 180 VADICK STREET  
11 CITY: New York  
12 STATE: New York  
13 COUNTRY: U.S.A.  
14 ZIP: 10014

COMPUTER READABLE FORM:  
1 MEDIUM TYPE: floppy disk  
2 COMPUTER: IBM PC COMPATIBLE  
3 OPERATING SYSTEM: PC DOS/MS-DOS  
4 SOFTWARE: PATENT RELEASE #1.0, Version #1.25  
5 CURRENT APPLICATION DATA:  
6 APPLICATION NUMBER: US/09/01408  
7 FILING DATE: 11-Jul-2001

CLASSIFICATION: (Unknown)  
1 APPLICATION DATA:  
2 FILING DATE: 07/07/95  
3 APPLICATION NUMBER: US 07/496 397  
4 FILING DATE: 26-JUN-1992  
5 APPLICATION NUMBER: US PCT/US92/05401  
6 FILING DATE: 26-JUN-1992  
7 FILING DATE: 15-APR-1992  
8 APPLICATION NUMBER: US PCT/US92/02750  
9 FILING DATE: 02-APR-1992  
10 APPLICATION NUMBER: US 07/413 593  
11 FILING DATE: 24-DEC-1991  
12 APPLICATION NUMBER: US 07/793 365  
13 FILING DATE: 15-NOV-1991  
14 APPLICATION NUMBER: US 07/728 913  
15 FILING DATE: 28-JUN-1991  
16 APPLICATION NUMBER: US 07/673 666  
17 FILING DATE: 02-APR-1991

ATTORNEY/AGENT INFORMATION:  
1 NAME: Feit, Irvin N.  
2 REGISTRATION NUMBER: 28 601  
3 REFERENCE/DOCKET NUMBER: LEM-1-7P  
4 TELECOMMUNICATION INFORMATION:  
5 TELEPHONE: 212-645-1405  
6 TELEFAX: 212-645-2054

INFORMATION FOR SEQ ID NO: 2:  
1 SEQUENCE CHARACTERISTICS:  
2 LENGTH: 992 amino acids  
3 TYPE: amino acid

US-09-919-408-4

Result	Query No.	Score	Query Length	DB Length	ID	Description
1	1	38	97.4	1004	2	138074
2	2	37	94.9	508	2	921654
3	3	36	92.3	208	2	874605
4	4	35	89.7	539	2	888967
5	5	34	87.2	530	2	782061
6	6	34	87.2	780	2	058465
7	7	34	87.2	1611	2	178276
8	8	33	84.6	227	2	682118
9	9	33	84.6	227	2	570072
10	10	33	84.6	737	2	134964
11	11	33	84.6	214	2	529810
12	12	33	84.6	514	2	439368
13	13	33	84.6	517	2	547138
14	14	33	84.6	517	2	246385
15	15	33	84.6	514	2	071082
16	16	33	84.6	982	2	633551
17	17	33	84.6	818	2	79120
18	18	33	84.6	2819	2	850551
19	19	31	84.6	3157	2	970969
20	20	31	84.6	269	2	650445
21	21	32	82.1	269	2	875397
22	22	32	82.1	361	2	686239
23	23	32	82.1	361	2	686239
24	24	32	82.1	422	2	575155
25	25	32	82.1	422	2	575155
26	26	32	82.1	445	2	071192
27	27	32	82.1	445	2	60556
28	28	32	82.1	507	2	726809
29	29	32	82.1	513	2	826190

Query Match	54.9%	Score 37	DB 2	Length 602
Best Local Similarity	55.7%	Pred. No. 19		
Matches	6	Conservative	0	Indels 0
		Mismatches	0	Gaps 0

QY 1 STGYPLP 7  
DB 456 SVGYPLP 472

RESULT 5  
A72405  
Conserved hypothetical protein - Thermococcus maritima (strain MSB)  
C:Species: Thermococcus maritima  
C:Date: 11-Jun-1995 #sequence\_revision 11-Jun-1999 #text\_change 21-Oct-2000  
C:Accession: A72405  
R:Wilson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, M.J.; Dodson, R.; Nelson, K.E.; Stewart, A.M.; Chilton, M.D.; Pratt, M.S.; Phillips, R.A.; Richardson, D.D.  
N:Gene 399, 315-329, 1999  
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria: a new domain  
A:Reference number: A72200; PMID:99287316; PMID:10760521  
A:Accession: A72405  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-205 (AAR)  
A:Cross-references: GB:AE001705; GB:AE000512; MID:04906594; PDB:AA15249 1; PDB:049070  
A:Experimental source: strain MSB  
C:Genetics: JMC207  
C:Superfamily: conserved hypothetical protein MJ1163

Query Match 92.3% Score 36; DA 2; Length 206;  
Best Local Similarity 71.4%; Pred. No. 9.4;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 STGYPLP 7  
DB 28 SVGYPLP 34

RESULT 4  
B89947  
serine proteinase spIC (amorted) - Staphylococcus aureus (strain N315)  
C:Species: Staphylococcus aureus  
C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 21-Oct-2002  
C:Accession: B89947  
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Oji, L.; Oda, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratsuka, K.  
N:Title: Whole genome sequence of methicillin-resistant Staphylococcus aureus.  
A:Reference number: B89736; PMID:11418145  
A:Accession: B89947  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-239 (KUN)  
A:Cross-references: GB:BAC00318; PDB:1H7D1504; PDB:BAB4297 1; USFCA:080214  
A:Experimental source: strain N315  
C:Genetics:  
C:Superfamily: Staphylococcal serine proteinase

Query Match 85.7% Score 35; DA 2; Length 239;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SVGYPLP 7  
DB 155 ISGYPLP 160

RESULT 5  
D82003  
thiamin ABC transporter, permease protein VC2539 (amplified, - Vibrio cholerae)  
C:Species: Vibrio cholerae  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2003 #text\_change 02-Feb-2003

C:Accession: B82003  
R:Kienleberg, C.F.; Eisen, J.A.; Nelson, M.C.; Clayton, R.A.; Gwin, M.L.; Dodson, M.J.; Dodson, R.; Wilson, K.E.; Stewart, A.M.; Chilton, M.D.; Pratt, M.S.; Phillips, R.A.; Richardson, D.D.  
N:Gene 406, 172-183, 2003  
A:Title: DNA sequence of both chromosomes of the Vibrio pathogen Vibrio cholerae.  
A:Reference number: B82003; PMID:12406433; PMID:10952303  
A:Accession: B82003  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-550 (HES)  
A:Cross-references: GB:AE01321; GB:AE01554; MID:049657119; PDB:AMP95679 1; GSPEN  
A:Experimental source: strain N1651; biotype 51 for  
C:Genetics: JMC133  
A:MAP position: 1

Query Match 87.2% Score 34; DA 2; Length 530;  
Best Local Similarity 71.4%; Pred. No. 55;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 STGYPLP 7  
DB 119 SVGYPLP 125

RESULT 6  
D69855  
conserved hypothetical protein ykuo - Bacillus subtilis  
C:Species: Bacillus subtilis  
C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 15-Oct-1999  
C:Accession: D69855  
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; B.  
C:Phillips, S.D.; Emerson, P.T.; Ehteshami, K.B.; Farrington, J.; Gabret, C.; Ferrari  
N:Gene 190, 249-256, 1997  
A:Title: ykuo, a conserved hypothetical protein in Bacillus subtilis.  
A:Reference number: D69855  
A:Accession: D69855  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-760 (KUN)  
A:Cross-references: GB:059117; GB:ALC09126; MID:02633695; PDB:1CAB13280 1; PDB:118  
A:Experimental source: strain 168  
C:Genetics:  
A:Superfamily: ykuo

Query Match 87.2% Score 34; DA 2; Length 760;  
Best Local Similarity 71.4%; Pred. No. 97;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVGYPLP 7  
DB 456 SVGYPLP 462

RESULT 7  
B82003  
hypothetical protein BAC20A17 - Escherichia coli (Shiga toxin-producing E. coli)  
C:Species: Escherichia coli  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2003 #text\_change 01-Dec-1999  
C:Accession: B82003  
R:Kurayama, K.; Harris, D.; Ward, V.; Barrell, B.G.; Rajandream, M.A.





R.Peter, D.; Finn, J.E.; Kisek, I.; Liu, Y.; Kozls, T.; Hagenmann, C.; Reimann, A.; Spd  
Genetics 16, 720-723, 1993.  
A:Species: *Rattus norvegicus*  
A:Accession: A49368; NCID:9414368; PMID:1505809  
A:Status: Preliminary  
A:Molecule type: nucleic acid sequence not shown, cdt compared with neuronal T14  
A:Residues: 1-514 <ERR>  
P.Erickson, J.D.; Eiden, D.E.  
J. Neurochem. 61, 2314-2317, 1993  
A:Title: Functional identification and molecular cloning of a human brain vesicle monoamine transporter  
A:Reference number: JN5825; NCID:9406582; PMID:845493  
A:Molecule type: mRNA  
A:Accession: A49368  
A:Residues: 1-514 <ERR>  
A:Cross-references: GB:U23403; NCID:9439711; PID:AA61290.1; PID:9439712  
R.Lesch, K.P.; Gross, J.; Wolozin, B.L.; Murphy, D.L.; Riederer, P.  
J. Neural Transm. 93, 75-82, 1994  
A:Title: Extensive sequence divergence between the human and rat brain vesicular monoamine transporter  
A:Reference number: 139281  
A:Accession: U39281  
A:Molecule type: mRNA  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Residues: 1-516, H, 18-514 <RUS>  
A:Cross-references: EMBL:X71554; NCID:9266188; PID:CA55045.1; PID:9439459  
C:Comments: This protein allows neurotransmitters to be accumulated from the cytor.asm in  
A:Gene: VMAT2; VAT2; SVAT  
A:Map position: 10q25  
C:Superfamily: synaptic vesicle amine transporter  
A:Keywords: glycoprotein; phosphoprotein; transmembrane protein  
F121-44/Domain: transmembrane status predicted <TM>  
F130-151/Domain: transmembrane status predicted <TM>  
F160-179/Domain: transmembrane status predicted <TM>  
F190-210/Domain: transmembrane status predicted <TM>  
F292-311/Domain: transmembrane status predicted <TM>  
F328-352/Domain: transmembrane status predicted <TM>  
F358-378/Domain: transmembrane status predicted <TM>  
F388-410/Domain: transmembrane status predicted <TM>  
F417-437/Domain: transmembrane status predicted <TM>  
F446-470/Domain: transmembrane status predicted <TM>  
F15.18.279/Binding site: phosphate (Ser) (covalent) (by protein kinase C) status predicted  
F153.496/Binding site: phosphate (Thr) (covalent) (by protein kinase A) status predicted  
F416/Binding site: phosphate (Ser) (covalent) (by protein kinase A) status predicted  
Query Match 84.6%; Score 33; DB 2; Length 514;  
Best Local Similarity 83.3%; Pred. No. 1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 2 ICYPLP 7  
DB 155 ICYPLP 162  
RES027 13  
A46374  
A:Title: Rat vesicular monoamine transporter - rat  
C:Species: *Rattus norvegicus* (Norway rat)  
C>Date: 21-Sep-1993; sequence revision 19-Nov-1994; text change 17-Nov-2000  
A:Accession: A46374; B43319; text change 17-Nov-2000  
P.Erickson, J.D.; Eiden, D.E.; Hoffman, B.J.  
Proc. Natl. Acad. Sci. U.S.A. 86, 10993-10997, 1989  
A:Title: Expression cloning of a reserpine-sensitive vesicular monoamine transporter  
A:Reference number: A46374; NCID:94066370; PMID:1436194  
A:Accession: A46374  
A:Status: Preliminary  
A:Molecule type: nucleic acid  
A:Residues: 1-515 <ERR>  
A:Cross-references: NCID:9439454; PID:AA61162.1; PID:9439717  
A:Notes: Sequence extracted from NBT backbone (NCBI:114297); NBT:114297  
R.Liu, Y.; Peter, D.; Raghani, A.; Schildner, S.; Priyo, G.G.; Fischberg, D.; Reimann, N.  
Cell 70, 539-551, 1992

A:Title: A cDNA that suppresses MHV-1 toxicity encodes a vesicular amine transporter  
A:Reference number: A46374; NCID:9439717; PMID:1505825  
A:Species: *Rattus norvegicus*  
A:Accession: A46374  
A:Molecule type: mRNA  
A:Residues: 1-515, K, 122-515, 120-  
A:Notes: Sequence extracted from NBT backbone (NCBI:114297); NBT:114297  
C:Superfamily: synaptic vesicle amine transporter  
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Best Local Similarity 83.3%; Pred. No. 1e+02;  
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QY 2 ICYPLP 7  
DB 155 ICYPLP 162  
RES027 14  
S41061  
A:Title: Monoamine transport protein 2, vesicular - bovine  
A:Species: *Bos primigenius taurus* (cattle)  
C>Date: 25-Dec-1994; sequence revision 05-Apr-1995; text change 24-Sep-1993  
A:Accession: S41061; S39440; S39441; A4205  
P.BS Left 334, 56-22, 1994  
A:Title: Cloning and functional expression of a tetrahydrozine sensitive vesicular m  
A:Reference number: S41061; NCID:9439488; PMID:8107150  
A:Accession: S41061  
A:Residues: 1-517 <RUS>  
A:Molecule type: mRNA  
A:Cross-references: GB:U23476; NCID:9439717; PID:AA61833.1; PID:9410688  
A:Experimental source: adrenal medulla  
R.Krejci, P.; Gagliardi, B.; Bottom, D.; Isambert, M.F.; Sayne, C.; Gagnon, J.; Masson  
Proc. Natl. Acad. Sci. U.S.A. 89, 9730-9734, 1992  
A:Title: Expression and regulation of the bovine vesicular monoamine transporter ge  
A:Reference number: S39440; NCID:94063073; PMID:7902299  
A:Accession: S39440  
A:Molecule type: mRNA  
A:Residues: 1-527, T, 54-181, S, 155-464, S, 466, F, 467-473, SRS, 477-517 <RUS>  
A:Cross-references: GB:X76380; NCID:9457485; PID:CA53970.1; PID:9457485  
A:Accession: S39441  
A:Molecule type: protein  
A:Experimental source: adrenal medulla  
R.Krejci, P.; Gagliardi, B.; Bottom, D.; Isambert, M.F.; Sayne, C.; Gagnon, J.; Masson  
Proc. Natl. Acad. Sci. U.S.A. 89, 9730-9734, 1992  
A:Title: Homology of a vesicular amine transporter to a gene conferring resistance  
A:Reference number: A47205; NCID:93286316; PMID:1357568  
A:Accession: A47205  
A:Molecule type: protein  
A:Residues: 3-13, X, 21-28, X, 39-294-295, C, 297-300, K, 302 <STE>  
A:Experimental source: adrenal medulla  
A:Note: sequence modified after extraction from NBT backbone  
C:Comments: VMAT2  
A:Superfamily: synaptic vesicle amine transporter  
C:Keywords: glycoprotein; membrane protein  
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DB 155 ICYPLP 164  
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A:Status: Preliminary  
A:Molecule type: nucleic acid  
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A:Cross-references: NCID:9439454; PID:AA61162.1; PID:9439717  
A:Notes: Sequence extracted from NBT backbone (NCBI:114297); NBT:114297  
R.Liu, Y.; Peter, D.; Raghani, A.; Schildner, S.; Priyo, G.G.; Fischberg, D.; Reimann, N.  
Cell 70, 539-551, 1992

C:Species: Mus musculus (house mouse)  
C:Date: 10-Sep-1999 (sequence revision 10-Sep-1999) atoxl\_etance 19-Jan-2001  
C:Accession: I48385; S21453  
C:Gene: RPLP0; ribosomal protein L0, P0  
C:GeneRef: 1; 195036; 1997A  
A:Title: High-level expression in male germ cells of testis for RNA helicase RPLP0.  
A:Reference number: I48385; MID:93148011; PMID 8445986  
A:Accession: I48385  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-514 <RES>  
A:Cross-references: EMBL:X65627; MID:951262; PIIN:CAA4581.1; PID:c11263  
C:Genetics:  
A:Gene: TNZ2  
C:Superfamily: ATP-dependent RNA helicase DBP  
C:Superfamily: ATP, nucleotide-binding: P-loop  
P:233-245/Region: nucleotide-binding motif A (P loop)  
P:244-249/Region: nucleotide-binding motif B  
P:248-251/Region: DEAD motif

Query Match: 94.6%; Score 13; DB 1; Length 514;  
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CY 2 ICYPLP /  
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1b 504 GTPAP 509

Search completed: October 2, 2003, 13:56:21  
Job time: 15 secs



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DR PR: T3674; T3674;
DR GenBank: SPAC13.03;
DR InterPro: IPR000000;
DR KEGG: 090000;
KW Hypothetical protein: Transmembrane
FT TRANSMEM 38 478
FT TRANSMEM 177 298
FT TRANSMEM 188 208
FT TRANSMEM 324 344
FT TRANSMEM 422 442
FT TRANSMEM 595 619
FT TRANSMEM 726 746
FT TRANSMEM 823 843
FT TRANSMEM 892 912
FT TRANSMEM 932 952
FT CARBOHYD 416 438
FT CARBOHYD 422 442
FT CARBOHYD 627 647
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Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1: SIGTFLP 7
DB 724 SVGTFLP 740

RESULT 2
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AC Q3JUE: 300; (Rel. 49; Created)
CT 16-SEP-2003 (Rel. 49; Last sequence update)
DT 15-SEP-2003 (Rel. 42; Last sequence update)
DE SH3 domain-binding glutamic acid-rich-like protein.
GN SH3GR1.
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
CX NCBI_Cxoid-10090;
RN 11
RP SEQUENCE FROM N.A.
RA Schaefer-Linert P., Bocz A., Naezayer M.
RA "Cloning the mouse Sh3-like protein from the human Sh3-like gene."
RA Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN 12;
RP SEQUENCE FROM N.A.
RC STRAIN: C57BL/6J; TISSUE: Hippocampus;
RX MEDLINE: 22354643; PUBMED: 12458581;
RA Okazaki Y., Futuno M., Kasakawa T., Adachi J., Bono H., Kondo S.,
RA Nishida K., Osato N., Saito K., Suzuki H., Yanaka H., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nozaki A., Schonbach G., Gotoh T.,
RA Baldarelli R., Hill D.P., Holt C., Hume D.A., Quackenbush J.,
RA Schirra L.M., Knapin A., Matsuda H., Barshev S., Heisel K.W.,
RA Ball R., Bradt T.A., Bickel V., Chelha C., Corbani L.E., Cousens S.,
RA Datta R., Duan R., Eick J., Fiedler A., Fiedler K.,
RA Gaasterland T., Gariboldi M., Gissi C., Gocke A., Gocke J.,
RA Grimond S., Gustincich S., Hirokawa N., Jackson J.D., Jarvis L.D.,
RA Kanai A., Kawanishi K., Kawasaka Y., Kodziarski R.M., King B.L.,
RA Konegaya A., Kurochkin I.V., Lee Y., Lenhard R., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numa K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Portis J.C., Qi D., Ramachandran S.,
RA Ravasi I., Reed D.C., Reed D.C., Reid J., Ring B.Z., Ringold P.,
RA Saito R., Schneider C., Smith C.A., Smiton M., Shimada K.,
RA Sultana R., Tashiro H., Tashiro H., Tashiro H., Tashiro H.,
RA Vitarino L.G., Wyszewski A., Yanagisawa M., Yang L., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

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HA Hirozumi Kishikawa T., Kono H., Nakanura M., Sakazume N., Sato K.,
HA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
HA Mura K., Masuzume W., Imoto K., Ishii Y., Itoh M., Kiyawa T.,
HA Yashima A., Yoshino M., Yoshida K., Shiba K., Shingaya T.,
HA Hayashi K., Hayashizaki Y., Watanabe R., Linder E.S., Rogers J.,
HA "Analysis of the mouse transcriptome based on functional annotation of
HA 63,770 full-length cDNAs."
HA Nature 420:563-573(2002).
RN 13;
RP SEQUENCE FROM N.A.
RC STRAIN: C57BL/6J; and FVB/N; TISSUE: Brain;
RX MEDLINE: 22354557; PUBMED: 12477432;
RA Strausberg S.L., Feingold E.A., Grouse L.H., Berger G.,
RA Altshuler S.L., Brown J.S., Chen J., Chen M., Chen Y.,
RA Altschul S.F., Beckwith B., Buetow K.H., Schaefer C.F., Scher N.K.,
RA Hopkins R.F., Jarman M., Kaeber T., Max S.I., Wang J., Hsieh F.,
RA Stachenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Boudreau M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein W.J., Udell T.B., Toshiyuki S., Carninci P., Mullany S.J.,
RA Rhee S.S., Loisel N.A., Peters G.J., Abramson R.D., Mullen J.,
RA Roark S.A., McEwen P., McKernan K.J., Malek J.A., Gunatillake P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Kelly S.W.,
RA Villanar F.K., Munz T.K., Sodergren E.J., Lu X., Gibbs R.A., Chuz S.,
RA J. M. Venter A., Yavor A.C., Shchurtenko Y., Bouffard G.C.,
RA Plessley R.A., Tringali J.M., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Tringali J.M., Schmutz J., Myers K.M.,
RA Pattersonfield Y.S.N., Krzywicki M.T., Skalska U., Smalusz D.F.,
RA Schumacher A., Schein M.E., Jones S.M., Marra M.A.,
RA "Genomic and initial analysis of more than 15,000 full-length
RA human and mouse cDNA sequences."
RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN 14;
RP SIMILARITY: BELONGS TO THE SH3R1 FAMILY.
CC THIS SWISS-PROT entry is copyrighted by the Swiss Institute of Bioinformatics.
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CC activities requires a license agreement (See http://www.isb.ch/procure/
CC or send an email to licensing@isb.ch).
RN 15;
RP FHL1: A27534; CAB764.9.1;
RN 16;
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RESULT 6			
VMT2.HUMAN	STANDARD:	PRT:	514 AA.
AC Q35942.Q35876:			
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DT C1-CHT-1994 (Ref. 1C, Last sequence update)			
DT 24-FEB-2003 (Ref. 01, Annotation update)			
DE SYNAPTIC vesicle amine transporter (Mucamine transporter) (Vesicular			
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CS Homo sapiens (Human).			
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
CC NCP--Xenit-9676;			
CC EXPULSION FROM NA			
EX NCT-1NR-Q37564; PFMW-405030;			
EX SURFAT K.K., POSSICA A.M., YANG X.D., EDGAR S.P., BIRD G.S.,			
EX HEALING A.B., GRATTIN C.A., LI X., DABS R.W., UHL G.R.;			
KA "A human synaptic vesicle mucamine transporter cDNA predicts			
KC posttranslational modifications," REVEALS CHROMOSOME 10 GENE			
KI LOCALIZATION AND IDENTIFICATION USING MRPs."			
RI PERS Lett. 318:115-136(1993).			
RN 125-BENT FLOW N-A			
EN 125-BENT FLOW N-A			
EX SEDU-NP-H060520; PUBMED-245963.			
EX ERICKSSON J.O., PEDERSEN E.			
BT Functional identification and molecular cloning of a human brain			
BT vesicular mucamine transporter."			
PN J. Neurochem 61:2311-2317(1993).			
PK [1]			
RC EXPULSION FROM NA.			
RC TISSUE-Substantia nigra;			
RC Nucleus accumbens (NAc);			
RC Putamen (PUT). FOR J.P.P., EDWARDS R.H.			
PA Submitted (MAR 1996) TO THE SWISS/GENBANK/UCSC databases.			
PA EXPULSION FROM NA.			
PC SOURCE: PFM N.A.			
KC TISSUE=brain.			
RA LUSCH K.B., GROSS J.J., WELZIN B.L., MURPHY D.L., KIEDERER P.;			
RA "Extensive sequence divergence between the human and rat brain			
RC vesicular mucamine transporter: possible molecular basis for species			
RC difference in the susceptibility to MP-7."			
KL J. Neural. Transm. 93:75-82(1993).			
KN C-SOLUTE BIND.			
EX SEDUINE-2230784; PFMW-120C4896;			
EX THURIEL D.S., STEVENS M.K., RUOHO A.E.			
BT Identification of human vesicle mucamine transporter (VMA12);			
BT lumenal cysteines that form an intramolecular disulfide bond *;			
RI Biochemistry 41:6346-6353(2002).			
CC -FUNCTION INVOLVED IN THE ATP-DEPENDENT VESICULAR TRANSPORT OF			
CC BIOGENIC AMINE NEUROTRANSMITTERS. REQUIREMENT FOR VESICULAR AMINE			
CC STORAGE PRIOR TO SECRETION VIA EXOCYTOSIS.			
CC SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. VESICULAR			
CC SIMILARITY: STRONG WITH CHROMAFIN GRANULE AMINE TRANSPORTER AND			
CC TO INTERFERE VESICULAR ACETYLCHOLINE TRANSPORT.			
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CC EMBL_199118; AAA59877.1.			
DB			

DR EMBL: L23205; AA61290.1 (1)  
DR EMBL: L14269; AA91851.1 (1)  
DR EMBL: X71354; CA50459.1 (1)  
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DR CUS: S29810; S29810; SCL18A2  
DR MW: 19330; C13935; SCL18A2  
DR GO: GO:0005687; Cytosol to plasma membrane; TAS  
DR GO: GO:0005624; C-membrane fraction; TAS  
DR GO: GO:0005803; Secretory vesicle; TAS  
DR GO: GO:0008504; P-monomamine transporter activity; TAS  
DR GO: GO:0015844; P-monomamine transporter; TAS  
DR InterPro: IPR007114; NES  
KW Transport; Transmembrane; Glycoprotein; Neurotransmitter transport;  
KW Phosphorylation;  
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FT MOD\_RES 513 513 PHOSPHORYLATION (BY CK2) (BY SIMILARITY);  
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FT CONFLICT 302 302 C -> S (IN REF. 1);  
FT CONFLICT 354 354 K -> T (IN REF. 1);  
FT CONFLICT 378 378 A -> P (IN REF. 1);  
FT CONFLICT 395 395 I -> N (IN REF. 1);  
FT CONFLICT 514 514 I -> N (IN REF. 1);  
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Db 156 IGPP 161  
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DI 01-JUL-1993 (Rel. 26, last sequence update)  
DI 28-FEB-2003 (Rel. 41, last annotation update)  
DE Synaptic vesicle amine transporter (Monamine transporter) (Vesicular  
amine transporter 2) (VAT2)  
GN SLC18A2 OR VAT2 OR SVAT  
OS Rattus norvegicus (Rat.)  
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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CC NCBI\_Taxid: 10116;  
PR 11  
RP SEQUENCE FROM N.A.  
RX MEDLINE: 9276677; PubMed: 1504242;  
RX EMBL: X71354; CA50459.1 (1)  
KA Blomberg J.D., Kachadourian R.M.  
KA A CNA that suppresses MEPA toxicity encodes a vesicular amine  
transporter.  
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[illegible]



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Query Match: 82.18 Score 32. DB 1. Length: 385:
Best Local Similarity: 83.38: Freq: No. 58:
Matches: 51: Conservative: 11: Mismatches: 9: Indels: 9: Gaps: 0:

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DQ      325 107EVP 330

RESULT 13
TAG CALED      STANDARD:      PRT: 507 AA.
1C  TAG CALED.
1D  15-SEP-2003 (rev. 42, Created)
1E  15-SEP-2003 (rev. 42, Last sequence update)
1F  15-SEP-2003 (rev. 42, Last annotation update)
1G  Functional-Tox Protein 33.
1H  TBX-33 OR V6A7A.8.
1I  Cancerbiondilis elegans.
1J  Fukuoka: Metazoa: Nematoda: Chromadorea: Rhabditidae: Rhabditoidae:
1K  Rhabditidae: Polidreinae: Caenorhabditis.
1L  CH_TBX33-4239.
1M  CH_TBX33-4239.
1N
1O
1P  SEQUENCE FROM N.A.
1Q  STRAIN: Bristol N2.
1R  STEWARD: C. A. Metchnikoff. L. Souton J.F.
1S  Submitted (02-1998) to the EMBL/GenBank/DBJ databases.
1T  (2)
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1V  Arthur R. (1970-2001), to the EMBL/GenBank/DBJ databases.
1W  Submitter: NCAR, LOCATION: Unpublished (Confidential).
1X  1-1: SIMILARITY: Contains 11: 100: domain.
1Y
1Z
2C  THIS SWISS-PROT entry is copyright. It is produced through a collaboration
2D  between the Swiss Institute of Bioinformatics and the EMBL outstation
2E  the European Bioinformatics Institute. There are no restrictions on its
2F  use by non-profit institutions as long as its content is in go way
2G  modified and this statement is not removed, please by and for commercial
2H  or social request to the EMBL outstation (See http://www.ebi.ac.uk/andouche/)
2I  or social request to the EMBL outstation.
2J
2K  EMBL: AL032622; CAZ21503.1;
2L  EMBL: AL032622; CAZ21503.1; JOINED.
2M  EMBL: AL590412; CAZ21502.1;
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CC ENML AC0584; AAAS6907;
CC DR AKR057; CAQ21574;
CC ENBL S54224; CAS1864;
CC DR PTP; B26169; B26190;
CC DR SUB; List; B31649; gntS;
CC DR InterPro: IPRO05577; PCY xln;
CC DR InterPro: IPRO06062; Glucuronate kinase
CC DR Pfam: PF0370; PCY; 1
CC DR Pfam: PF0792; PCY; 1
CC DR GORFAM: NS000111; GORF; 1
CC DR PRESITE: PS00913; PCY-X-NAZE; 1
CC DR Glucose utilization; Transferase; Kinase; Complete proteome
CC SQ SEQUENCE: 513 AA, 57155 MW, 3510410.407AC3ED CRC64;

Query Match      92.1%   Score 32    E 1    Length 913.
Eust Local Similarity: 103.0%   Pred. No. 78;
Matches          C: Conservative    D: Mismatches    C: Indels    C: Gaps

CY       1 NLYVL 6
OD       31 KSYPL 65

RESULT 15
CAR2_AQUIAE STANCAP; PRO: 547 AA.
ID CAR2_AQUIAE
NC 567213;
AT 24-FEB-2003 (Pct: 41; Grnded)
DT 24-FEB-2003 (Gr: 41; Last sequence update)
DE Carboxyl-phosphate synthase large chain (C-terminal section)
DE (EC 4.3.5.5) [Carbamoyl-phosphate synthetase ammonia chain].
DN CAPH2 OR AL1192
DS Aquifex aeolicus
GS Aquifex aeolicus
OS Aquifex aeolicus
RA Gehrig A.; Aquilicon; Aquificales; Aquificaceae; Aquifex.
CX NCBI_TaxId=63361;
GX (1)
RP SEQUENCE FROM N.A.
RF RefSeq: NC_031866; PubMed=937720;
RA Seibert J.E., Warren P.W., Gaasterland T., Young W.G., Leroux A.L.,
RA Geelan D.E., Overbeek R., Snead M.A., Keller M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Sanson R.V.;
RA "The complete genome of the hyperthermophilic bacterium Aquifex
RA aeolicus".
RC Nature 392:333-338(1998).
CC -- CATALYTIC ACTIVITY: 2 ATP + L-glutamate + CO(2) -> H(2)O + 2 ADP +
CC -- Phosphate + L-glutamate + carbamoyl phosphate (by similarity);
CC -- PHOSPHATE: 10.0 moles per mole substrate per minute (by similarity);
CC -- PATHWAY: Arginine biosynthesis;
CC -- PATHWAY: Pyrimidine biosynthesis; first step.
CC -- SUBUNIT: Composed of two chains: the small (for 4-uracine) chain
CC promotes the hydrolysis of glutamine to ammonia, which is used by
CC the large (or ammonia) chain to synthesize carbamoyl phosphate (by
CC similarity);
CC -- SIMILARITY: BELONGS TO THE CARB FAMILY. C-TERMINAL SECTION.
CC -- CATION: Sequence of CARB is split into two genes in A.aeolicus
CC (AAC1112 and AQ2103).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announcements
CC or send an email to licensel@isb-sib.ch).
CC ENBL AC0584; CAQ21574;
CC DR AKR057; CAQ21574;
CC DR BSSP; PC0965; IBMK
CC HAMAP; MF 01210; ATYP; 041 1

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DR InterPro: PRO3463; CpsA_L.
DR InterPro: PRO3469; CpsA_L_D2.
DR InterPro: PRO3481; CpsA_L_N.
DR InterPro: PRO3482; MOS_Like.
DR Pfam: PF02389; CpsA_L_Cat1; 1.
DR Pfam: PF02386; CpsA_L_D2; 1.
DR Pfam: PF02142; MGS; 1.
DR PRINTS: PRO3098; CpsA.
DR PROSITE: PS00866; CpsA.1; 1.
DR PROSITE: PS00867; CpsA.2; 1.
KW Arginine biosynthesis; Pyrimidine biosynthesis; Cysase; ATP-Ligase;
KW Manganese; Complete proteome.
FT DOMAIN 1 397 CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
FT METAL 398 537 ALLOSTERIC DOMAIN.
FT METAL 272 484 MANGANESE 3 (BY SIMILARITY).
FT METAL 344 484 MANGANESE 4 (BY SIMILARITY).
SQ SEQUENCE 537 AA; 80037 MW; 9C77F62F088656 ERS04.

Query Match 82 %; Score 32; DB 1; Length 537.
Seq. Local Similarity 100.0%; Pred. No. 82.
Matches 6; Conservative 0; Mismatches 0; Gaps 0.

QY 1 STRIP: 6
2b 1 1 1
2b 236 SIGYPS 304

Search completed: October 2, 2003, 13:55:19
Job time : 13 sec
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DB 494 S3VPLP 472

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RESULT 2
AC Q9MY50 PRELIMINARY: PRT: 208 AA.
DT 01-NOV-1999 (TRENBLER, 12, Created:
DT 01-NOV-1999 (TRENBLER, 12, Last sequence update)
DT 01-MAR-2002 (TRENBLER, 20, Last annotation update)
DE Hypothetical protein TMO207.
OS Thermococcus maritima.
OC Bacteria; Thermococcales; Thermococcaceae; Thermococcus.
ON NCBI-TaxID=3350.
LN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=MS8 / DSM 3103.
RX MEDLINE=9528736, PubMed=10360571.
RA Nelson K.E., Clayton R.A., Gill S.R., Swine M.L., Dodson R.J.,
RA Matt D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L., Uitterlinden T.R., Nakajima J.A., Linner K.D., Garrett W.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eison J.A., White O.,
RA Weidner J., Venter A., Adams M., Venter C.M., Fraser C.M.,
RT Evidence for lateral gene transfer between Archaea and Bacteria from
RT genome sequence of Thermococcus maritima.
RT Nature 399:323-329 (1999).
RL ENBL: A8001705; A8035299.1.
DR TIGR: TMO207.
DR Hypothetical protein; Complete proteome.
SQ SEQUENCE 208 AA; 23362 MW; 496A121599DD102F CRC64:
Query Match 92.38; Score 35; ES 16; Length 208;
Best Local Similarity 71.48; Pred. No. 37;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 S3VPLP 7
DB 2H S3VPLP 34

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DB 29 S3VPLP 35

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RESULT 4
AC Q9KH49 PRELIMINARY: PRT: 239 AA.
DT 01-NOV-1999 (TRENBLER, 15, Created:
DT 01-NOV-1999 (TRENBLER, 15, Last sequence update)
DT 01-MAR-2002 (TRENBLER, 24, Last annotation update)
DE Serine protease SPIC.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
ON NCBI-TaxID=1280.
LN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=8325-4.
RX MEDLINE=2114646, PubMed=11179322.
RA Reed S.F., Wessol C.A., Liles F.F., Trimble W.R., Schlievert P.M.,
RA Holbach C.A., Hayes K.W.
RT Molecular Characterization of a Novel Staphylococcus aureus Serine
RT Protease Opened the Pathway to a Novel Serine Protease (SPIC).
RT Infect. Agents 5:151-152 (2001).
RC MEDLINE=157175, AAF57627.1.
DR TIGR: SPIC.
DR InterPro: IPR01940; Protrase20.
DR InterPro: IPR01454; Ser.protease_Try.
DR Pfam: PF03045; tryptic_1.
DR PRINTS: PRG0834; PROTEASES20.
DR PRINTS: PRG0835; V8PROTEASE.
DR SMART: SM00020; TYP_SEC_1.
DR PROSITE: PS00672; VE_HIS_1.
DR HydroLase: Protease; Serine protease.
SQ SEQUENCE 239 AA; 25098 MW; BA79FE1475692DBA CRC64:
Query Match 89.78; Score 35; DB 2; Length 239;
Best Local Similarity 100.00; Pred. No. 67;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 T3VPLP 7
DB 156 T3VPLP 180

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DB 494 S3VPLP 472

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RESULT 3
AC Q9R787 PRELIMINARY: PRT: 212 AA.
DT 01-NOV-1999 (TRENBLER, 21, Created:
DT 01-NOV-1999 (TRENBLER, 21, Last sequence update)
DT 01-MAR-2002 (TRENBLER, 21, Last annotation update)
DE Predicted Zn-dependent hydrolases of the beta-lactamase fold.
OS Thermobacterium tengcongensis.
OC Bacteria; Firmicutes; Clostridia; Thermobacteriales;
OC Thermobacteriaceae; Thermobacter.
ON NCBI-TaxID=119372.
LN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=MS8/2816 / DSM 11007.
RX MEDLINE=9528736, PubMed=11561395.
RA Bao Q., Tian Y., Li X., Xiao Z., Hu S., Dong W., Yang Z.,
RA Chen Y., Xue Y., Xu Y., Lei X., Huang H., Dong X., Xia Y., Ding L.,
RA Tan H., Chen R., Wang Z., Yang H., Yang H., Yang L.,
RA "A complete sequence of T. tengcongensis genome."
RL Genome Res. 12:689-700 (2002).
RC ENBL: AEU13175; AAK25651.1.
DR HydroLase: Complete Proteome.
SQ SEQUENCE 212 AA; 23845 MW; H26CJ0B6J0FTR51 CRC64:
Query Match 92.48; Score 35; ES 16; Length 212;
Best Local Similarity 71.48; Pred. No. 38;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 S3VPLP 7

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DB 29 S3VPLP 35

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RESULT 5
AC Q93782 PRELIMINARY: PRT: 239 AA.
DT 01-NOV-1999 (TRENBLER, 15, Created:
DT 01-NOV-1999 (TRENBLER, 15, Last sequence update)
DT 01-MAR-2002 (TRENBLER, 23, Last annotation update)
DE Novel antigen (Serine protease SPIC).
OS Staphylococcus aureus (strain M50 / ATCC 70659).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
ON NCBI-TaxID=1280, 158878, 158879, 1250.
LN (1)
RP SEQUENCE FROM N.A.
RC SPECIES=Staphylococcus aureus (ATCC 70659) (ATCC 70659);
RX MEDLINE=9741053, PubMed=944680.
RA Poretsky K., Rencoret J., Standaert M., Salasnik E., Bendizien K.,
RA "Molecular cloning and expression of a novel Staphylococcus aureus
RA antigen."
RC MEDLINE=158878, 158879, 1250.
DR TIGR: SPIC.
DR InterPro: IPR01940; Protrase20.
DR InterPro: IPR01454; Ser.protease_Try.
DR Pfam: PF03045; tryptic_1.
DR PRINTS: PRG0834; PROTEASES20.
DR PRINTS: PRG0835; V8PROTEASE.
DR SMART: SM00020; TYP_SEC_1.
DR PROSITE: PS00672; VE_HIS_1.
DR HydroLase: Protease; Serine protease.
SQ SEQUENCE 239 AA; 25098 MW; BA79FE1475692DBA CRC64:
Query Match 89.78; Score 35; DB 2; Length 239;
Best Local Similarity 100.00; Pred. No. 67;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 T3VPLP 7
DB 156 T3VPLP 180

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DB 494 S3VPLP 472

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RESULT 2
AC Q9MY50 PRELIMINARY: PRT: 208 AA.
DT 01-NOV-1999 (TRENBLER, 12, Created:
DT 01-NOV-1999 (TRENBLER, 12, Last sequence update)
DT 01-MAR-2002 (TRENBLER, 20, Last annotation update)
DE Hypothetical protein TMO207.
OS Thermococcus maritima.
OC Bacteria; Thermococcales; Thermococcaceae; Thermococcus.
ON NCBI-TaxID=3350.
LN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=MS8 / DSM 3103.
RX MEDLINE=9528736, PubMed=10360571.
RA Nelson K.E., Clayton R.A., Gill S.R., Swine M.L., Dodson R.J.,
RA Matt D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L., Uitterlinden T.R., Nakajima J.A., Linner K.D., Garrett W.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eison J.A., White O.,
RA Weidner J., Venter A., Adams M., Venter C.M., Fraser C.M.,
RT Evidence for lateral gene transfer between Archaea and Bacteria from
RT genome sequence of Thermococcus maritima.
RT Nature 399:323-329 (1999).
RL ENBL: A8001705; A8035299.1.
DR TIGR: TMO207.
DR Hypothetical protein; Complete proteome.
SQ SEQUENCE 208 AA; 23362 MW; 496A121599DD102F CRC64:
Query Match 92.38; Score 35; ES 16; Length 208;
Best Local Similarity 71.48; Pred. No. 37;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 S3VPLP 7
DB 2H S3VPLP 34

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DB 29 S3VPLP 35

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RESULT 4
AC Q9KH49 PRELIMINARY: PRT: 239 AA.
DT 01-NOV-1999 (TRENBLER, 15, Created:
DT 01-NOV-1999 (TRENBLER, 15, Last sequence update)
DT 01-MAR-2002 (TRENBLER, 24, Last annotation update)
DE Serine protease SPIC.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
ON NCBI-TaxID=1280.
LN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=8325-4.
RX MEDLINE=2114646, PubMed=11179322.
RA Reed S.F., Wessol C.A., Liles F.F., Trimble W.R., Schlievert P.M.,
RA Holbach C.A., Hayes K.W.
RT Molecular Characterization of a Novel Staphylococcus aureus Serine
RT Protease Opened the Pathway to a Novel Serine Protease (SPIC).
RT Infect. Agents 5:151-152 (2001).
RC MEDLINE=157175, AAF57627.1.
DR TIGR: SPIC.
DR InterPro: IPR01940; Protrase20.
DR InterPro: IPR01454; Ser.protease_Try.
DR Pfam: PF03045; tryptic_1.
DR PRINTS: PRG0834; PROTEASES20.
DR PRINTS: PRG0835; V8PROTEASE.
DR SMART: SM00020; TYP_SEC_1.
DR PROSITE: PS00672; VE_HIS_1.
DR HydroLase: Protease; Serine protease.
SQ SEQUENCE 239 AA; 25098 MW; BA79FE1475692DBA CRC64:
Query Match 89.78; Score 35; DB 2; Length 239;
Best Local Similarity 100.00; Pred. No. 67;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 T3VPLP 7
DB 156 T3VPLP 180

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DB 494 S3VPLP 472

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RESULT 3
AC Q9R787 PRELIMINARY: PRT: 212 AA.
DT 01-NOV-1999 (TRENBLER, 21, Created:
DT 01-NOV-1999 (TRENBLER, 21, Last sequence update)
DT 01-MAR-2002 (TRENBLER, 21, Last annotation update)
DE Predicted Zn-dependent hydrolases of the beta-lactamase fold.
OS Thermobacterium tengcongensis.
OC Bacteria; Firmicutes; Clostridia; Thermobacteriales;
OC Thermobacteriaceae; Thermobacter.
ON NCBI-TaxID=119372.
LN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=MS8/2816 / DSM 11007.
RX MEDLINE=9528736, PubMed=11561395.
RA Bao Q., Tian Y., Li X., Xiao Z., Hu S., Dong W., Yang Z.,
RA Chen Y., Xue Y., Xu Y., Lei X., Huang H., Dong X., Xia Y., Ding L.,
RA Tan H., Chen R., Wang Z., Yang H., Yang H., Yang L.,
RA "A complete sequence of T. tengcongensis genome."
RL Genome Res. 12:689-700 (2002).
RC ENBL: AEU13175; AAK25651.1.
DR HydroLase: Complete Proteome.
SQ SEQUENCE 212 AA; 23845 MW; H26CJ0B6J0FTR51 CRC64:
Query Match 92.48; Score 35; ES 16; Length 212;
Best Local Similarity 71.48; Pred. No. 38;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 S3VPLP 7

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DB 29 S3VPLP 35

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RESULT 5
AC Q93782 PRELIMINARY: PRT: 239 AA.
DT 01-NOV-1999 (TRENBLER, 15, Created:
DT 01-NOV-1999 (TRENBLER, 15, Last sequence update)
DT 01-MAR-2002 (TRENBLER, 23, Last annotation update)
DE Novel antigen (Serine protease SPIC).
OS Staphylococcus aureus (strain M50 / ATCC 70659).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
ON NCBI-TaxID=1280, 158878, 158879, 1250.
LN (1)
RP SEQUENCE FROM N.A.
RC SPECIES=Staphylococcus aureus (ATCC 70659) (ATCC 70659);
RX MEDLINE=9741053, PubMed=944680.
RA Poretsky K., Rencoret J., Standaert M., Salasnik E., Bendizien K.,
RA "Molecular cloning and expression of a novel Staphylococcus aureus
RA antigen."
RC MEDLINE=158878, 158879, 1250.
DR TIGR: SPIC.
DR InterPro: IPR01940; Protrase20.
DR InterPro: IPR01454; Ser.protease_Try.
DR Pfam: PF03045; tryptic_1.
DR PRINTS: PRG0834; PROTEASES20.
DR PRINTS: PRG0835; V8PROTEASE.
DR SMART: SM00020; TYP_SEC_1.
DR PROSITE: PS00672; VE_HIS_1.
DR HydroLase: Protease; Serine protease.
SQ SEQUENCE 239 AA; 25098 MW; BA79FE1475692DBA CRC64:
Query Match 89.78; Score 35; DB 2; Length 239;
Best Local Similarity 100.00; Pred. No. 67;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 T3VPLP 7
DB 156 T3VPLP 180

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[illegible]

DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DE 01-JUN-2002 (TrEMBLrel. 22, Last annotation update)  
DE Nucleotide protein.  
DE AT500460  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae.  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
CX NCBI\_TaxID=3702;  
CX [1];  
RN  
RP  
SEQUENCE FROM N.A.  
RA Yamada K., Hank J., Chan M.M., Chang C.H., Chang E., Dale J.V.,  
RA Tang C., Yoshida K., Yoshida K., Yoshida K., Yoshida K.,  
RA Tang C., Torii K., Torii K., Torii K., Torii K., Torii K.,  
RA Carlsberg P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,  
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,  
RA Meyers R.C., Miranda M., Nakasaka M., Nguyen M., Palm C.J.,  
RA Sakurai T., Sato M., Seki M., Shinozaki A., Shinozaki K.,  
RA Davis R.W., Ecker J.R., Ecker J.R., Ecker J.R., Ecker J.R.,  
RA "Arabidopsis Full Length cDNA Clones."  
RT Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
RN  
RP  
SEQUENCE FROM N.A.  
RA Yamada K., Hank J., Chan M.M., Chang C.H., Chang E., Dale J.V.,  
RA Tang C., Yoshida K., Yoshida K., Yoshida K., Yoshida K.,  
RA Tang C., Torii K., Torii K., Torii K., Torii K., Torii K.,  
RA Carlsberg P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,  
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,  
RA Miranda M., Nakasaka M., Nguyen M., Palm C.J., Sakurai T., Sato M.,  
RA Seki M., Shinozaki A., Shinozaki K., Shinozaki K., Ecker J.R.,  
RA Theologis A.  
RT "Arabidopsis Open Reading Frame (ORF) Clones."  
RC Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF092072; RAS13693.1;  
DR EMBL: AF122115; RAS13693.1;  
DR EMBL: AF122115; RAS13693.1;  
SQ  
SEQUENCE 918 AA: 104152 MW: D224C5B5A3B46A5C CAC64.  
Query Watch: 59.7%; Score 35; EB 10; Length 918;  
Best local similarity: 55.7%; Pred. No. 2.6e02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0.  
CY 1 SIGPIIP 7  
DB 871 SIGPIIP 677  
Search completed: October 2, 2003, 13:56:00  
Cdb time: 35 secs